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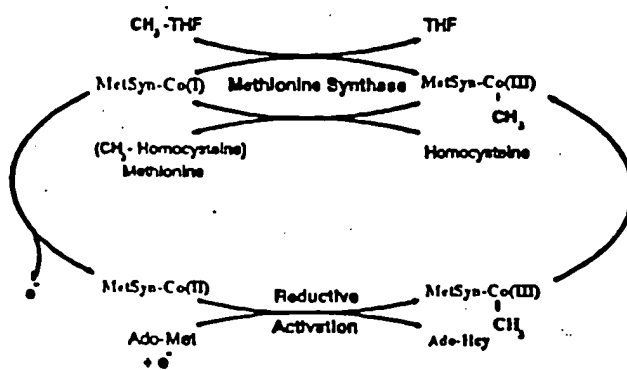


FIG. 1

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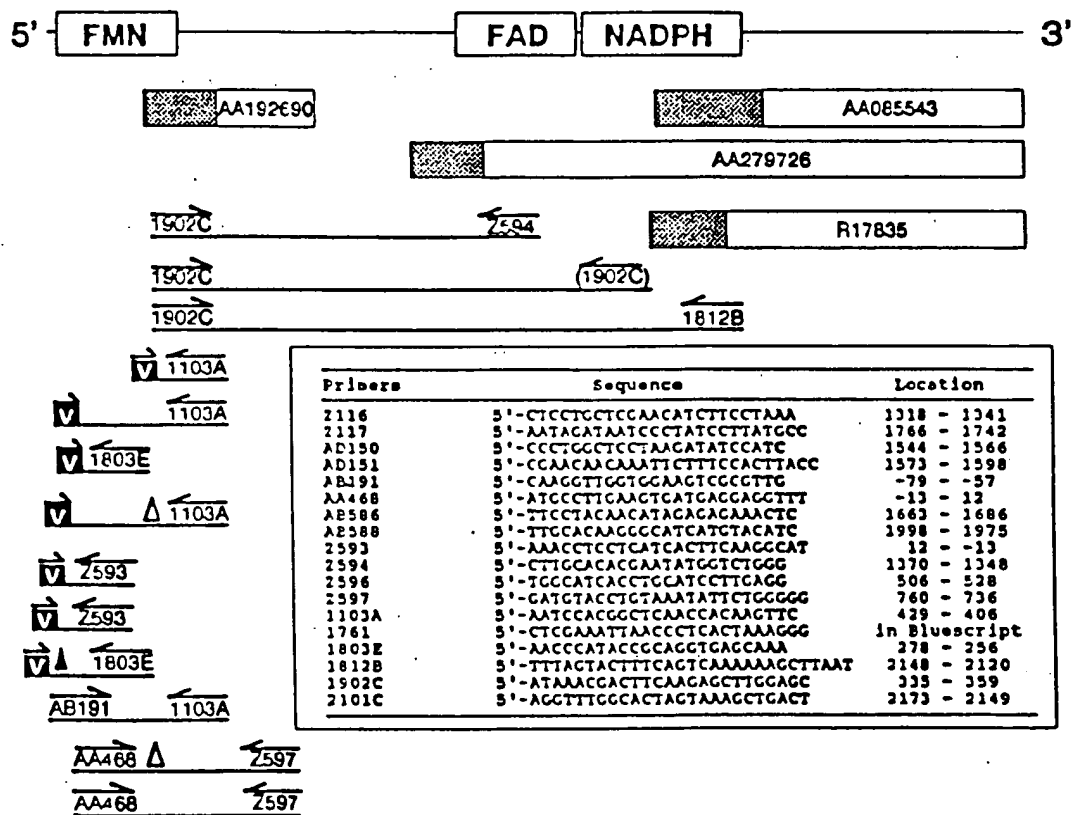


FIG. 2

CAAGGTTGGTGAAGTCCGTTGTGAGGTTCCGTGCCCGCTGGCGGGCGTGGTTCCTGTTACATGCCCTTGAAGTG
1 ATGAGGAGGTTTCTGTTACTATATGCTACACAGCAGGACAGGCAAGGCCATCGCAGAAGAAATGTGTGAGCAAGCTGTGGTACATGGATTTCTGCAGATCTTCACTGTAATTAGTGAA 40
MRRFLLLLYATOOQGA KAI A E E M C E Q A V V H G F S A D L H C I S E
121 TCCGATAAGTATGACCTAAAAACCGAAACAGCTCCCTTGTGTTGGTGTCTTACCCAGCGGACCGGACACACCGCCGCAAGTTTGTAAAGGAAATACAGAACCAACA 80
S D K Y D L K T E T A P L V V V S T T G T G D P P D T A R K F V K E I Q N O T
241 CTGCGGTTGATTTCTTGTCTACCTGCGGTATGGGTACTGGGTCTCGGTGATTGAGAATACACCTACTTTTGAATGGGGGCAAGATAATTGATAAACGACCTTCAAGAGCTTGGAGCC 120
L P V D F F A H L R Y G L L G L G D S E Y T Y F C N G G K I I D K R L O E L G A
361 CGGCATTTCTATGACACTGGACATGGAGTGTGTAGGTTTACAACCTGTGGTTGAGCGGTGGATTGCTGACTCTGCCAGCCCTCAGAAAGCATTITAGGTCAAGCAGAGGACAA 120
R H F Y D T G H A D D C V G L E L V V E P W I A G L V P A L R K H F R S S R G Q
481 GAGGAGATAAGTGGCGCAGTCCCGGTGGCATCCTTGCATCCTTGGAGCAGACACTTGTGAAGTCAGAGCTGCTACACATTGAATCTCAAGTCGAGCTTCTGAGATTGATGATTGAGGA 160
E E I S G A L P V A S P A S L R T D L V K S E L L H I E S Q V E L L R F D D S G
601 AGAAAGGATTCTGAGGTTTGAAGCAAAATGCACTGAACAGCAACCAATCAATGTTGTAAGAGCTTTGAGTCTCACTTACCGTTCCGTACCCCACTCTCACAAGCCTCTCTG 200
R K D S E V L K Q H A V N S H O S N V V I E D F E S S L T R S V P P L S Q A S L
721 AATATTCCTGGTTTACCCCAAGATATTTACAGGTACATCTGCAGGAGTCTTGGCCAGGAGCAAGCCAGTATCTGCACTTTCAGCAGATCCAGTTTTCAGTCCCAATTTCAGAG 240
N I P G L P P E Y L O V H L O E S L G O E S O V S V T S A D P V F Q V P I S K
841 GCAGTTCACCTTACTACCAATGATGCCATAAAACCACTCTGCTGGTACAATGGACATTTCAAAATACAGACTTTTCTATCAGCCTGGAGATGCCCTCAGCGTATCTGCCCTAACAGT 280
A V O L T T N D A I K T T L L V E L D I S N T D F S Y O P G D A F S V I C P N S
961 GATTCTGAGGTACAAGCCTACTCCAAGACTGCAGCTTGAAGATAAAAGAGAGGCACTGCTCTTTTGAATAAAGGAGCAGACACAAAGAAAGGAGCTTACCTTACCCAGCAGTATA 320
D S E V O S L L O R L O L E D K R E H C V L L K I K A D T K K K G A T L P O H I
1081 CCTGCGGGATGTTCTCTCCAGTTCATTTTTTACCTGGTGTCTTGAATCCGAGCAATTCCTAAAGAGGCAATTTTGGGAGCCCTTGTGGACTATACCAGTCACAGTTCAGAAAGCGCAGG 360
P A G C S L O F I F T W C L E I R A I P K K A F L R A L V D Y T S D S A E K R R
1201 CTACAGGAGCTGTGAGTAAACAGCGCGCAGGATTATAGCGCTTGTACGAGATGCCCTGTGCTGCTTGTGGATCTCTCTCTCGCTTCCCTTCTTGGCAGCCAGCAGTCTC 400
L O E L C S K O G A A D Y S R F V R D A C A C L L D L L L A F P S C O P P L S L
1321 CTGCTCGAATCTTCTTAACTTCAACCCAGACCATATTCGTGTGCAAGCTCAAGTTTATTTCAACCCAGGAAAGCTCCATTTTGTCTTCAACATTTGTGGAATTTCTGTCTACTGCCACA 440
L L E H L P K L O P R P Y S C A S S S L F H P G K L H F V F N I V E F L S T A T
1441 ACAGAGGTTCTCGGCAAGCGAGTATGTACAGGTGGCTGGCTTGTGGTGTCTTCACTTCTTCAACCAACATACATGCCATCCCATGAAGACAGCGGAAAGCCCTGGCTCCTAAGATA 480
T E V L R K G V C T G W L A L L V A S V L O P N I H A S H E D S G K A L A P K I
1561 TCCATCTCTCTCGAACAACAAATTTCTTCCACTTACCAGATGACCCCTCAATCCCATCATATGCTGGGTCAGGAACCGGCATAGCCCGTTTATGGGTCTTACAACATAGACAG 520
S I S P R T T N S F H L P O D D P S I P I I M V G P G T G I A P F I G F L O H R E
1681 AAATCCCAAGAACACCCAGATGCAAAATTTGGAGCAATGTGGTTGTTTTTGGCTCAGGCAAGGATAGGATTTCTATTTCAGAAAGAGCTCAGACATTTCCITTAAGCATGGG 560
K L O E O H P D G N F G A M W L F F G C R H K D R D Y L F R K E L R H F L K H G
1801 ATCTTAATCTCTAAAGTTTCTTCTCAAGAGATGCTCTGTTGGGAGGAGGAAGCCCCAGCAAGATGTACAAGACAACATCCAGCTTCTGCCCAGCAGGTGGCGAGAAATCCTC 600
I L T H L K V S F S R D A P V G E E A P A K Y V O D N I O L H G O O V A R I L
1921 CTCAGGAGAACGGGCATATTTATGTGTGTGGAGATGCAAGAATATGCCCAAGGATGTACATGATCCCTTGTGCAAAATAAAGCAAGAGGTTGGAGTTGAAAACTAGAAGCAATG 640
L O E N G N I Y V C G D A K N H A K D V H D A L V O I I S K E V G V E K L E A M
2041 AAAACCCCTGGCAGCTTTAAAAGAACAAAACCGTACCTTCAGGATATTTGCTCATAAACAGAAATTAAGAAAGAGGATTAAAGCTTTTTTGACTGAAGTACTAAAAGTCAGCTTTAC 680
K T L A T L K E E K R Y L O D I V S ***
2161 TAGTCCCAACCTTTAAATTTTCAAAACAAAATTTCTTCAACATTTCTTGAAGGACATGGAGTGGAGATTGGATCATTTTAAACAATAAACAAGCTTCTGATTGATTTTACGTATC 698
2281 TTTATCTACGCCCTTCTTGTGCTTGTGACTCTCCCAAAATTTGCCCTTGTGCTTGTGAGTCTTCTGAGCTAAAGGAGCCTTCACTCCCTATCAGCGCCTCTTACTTCCCAGAGAACT
2401 TCACAGAGACTCTGCTCTTCCATGCAAAAGGCTTCTTGAATAGGGAGAGCTGACTGAGTAGCTCATTTCTGTGACTTACAGTGCCAACTTTAAAAAGTATGAAATGATTTATTTT
2521 TATGATGATACCCATAAAGATGCTCATATTAATGTACTTAAATACACATGTAGAGCATATCTGTTATATGTTTATGTAACATCAAAATGGTTATTTGTTACTAAAGCTATATTTCTG
2641 AAAAAAATATTTAGGATAATTCCTACACAGGATTTATTTTATGATGCTGGGAAATATGAATGATTTTAAAAATTTCACTCTGGGCATATGGATTATCTATCACCATTACTTTT
2761 TTTAAGTCACAAATTCAGAAATTTGGGACATTTGCATTCATTTACAGGTACAGTACGTACATATTTAATAGAAAGATACAACCTTTTTTATTTTCACTCTTTTATTTCTGCTGCTT
2881 GGCACATTTTGTGTTTCCCACTATTTTGTCTCCATGATACCACTCAAGCAGTGTGCTGACCTAAAAATCTGACTTTAGTTAGTATCCTTGGATTTTATAGATTTCCCACTGCTCTAAT
3001 TCCCTGTTTATAATTTGCACAAACAAAACAAATGTTATGATAATCTTCTCCACTGTTCTAATATATATGTTATTTTATTTGATAGCTTGGGATTTAAACATCTCTGTTGAAGGCTTT
3121 TGATCCTTTTGAAGAAATAAGATCTGAAGAAATGGCATAATCTTAAAAAATAAAAA

FIG. 3 page 1 of 2

HsMTRR	
CeMTRR	
HsCPR	MGDSHVDTSSTVSEAAVEVSLSMTOMILFSLIVGLLTYWFLFRKKKEE	50
HsMTRRFMN.....	
CeMTRRMRRFLLLYATCGGCAKIAEEMCE	24
HsCPRMTDFLIATGCTGGAETIARSLKE	24
	VFETIKICTLTSVRESFVEKMKKTGRNIIIVYCSOTGTAEEFANRLSK	100
HsMTRRFMN.....	
CeMTRR	CAVVGCSADLNCISESDK-YDKT-----ETAPLVVVVSTGCGPP	66
HsCPR	NAELTGLTFRHLCENKKNLNE-----EKLC-AIVVESTGCGGAP	66
	DAHNYG----HRCMSADPEETOLADLSSLPEDNALVVFCHATTYCGOPT	146
HsMTRRFMN.....	
CeMTRR	CTAFKFKETONCTLPVDFFAHLRTGLLGLGSEYTYFCNGCKIIDKRLQ	116
HsCPR	DNCAPIVERINRNSLENEYLNLDYVLLGLGDSNYSTCTIFRDKOLT	116
	DNADDFYDVLCEQDVO---LSCVKFAVGLCKNTYENFNAMCKYVGRLE	193
HsMTRR	
CeMTRR	ELGARNFYDTGHADDVGLLELVPEWIAQLVAFALRKHFRSRCOEISGA	166
HsCPR	ALCANFLIGRAEADDVGLLELVPEWIEFFATLASRFDISADKHN----	162
	CLGACRIFELCLGDCGCHLEEDFITURECFUFAVCENF-----GV	233
HsMTRR	
CeMTRR	LPVASPALSRTDLVKSELLNIESOVELL--RFDCSGRCKSEVLKGNVNS	214
HsCPR	-ATTESENKLNKCVTE----EKKALLCKRIEDEESDDEGRGVIGID-	206
	EATGEESISCTEL-----VVHTDIDAARKVYMGEMRLASYEN	271
HsMTRR	
CeMTRR	NCSNVVIEDF---EESLTRSVPLS-CASLNIPGLPPEYLOVHLCESLGO	260
HsCPR	---MLIFENYDIFEISLLKGSOTLSNDEHLRVPAPGPFIVSSVSNEKLP	253
	CKP-----FFD-----AKNPFLLAAVTNRKLN	293
HsMTRR	
CeMTRR	EESCVS-----VTSADPVFCVPISKAVOLTY--NDAIKTLLVELDIS	301
HsCPR	EDIKLEUMLCKNFCVTKF FEVLVVSAEFVTDPTSKIRKMTVDG	303
	CGTE-----FNLHLELD	306
HsMTRR	
CeMTRR	N---TDFSTOFGCAFVVICPMSDSEVCSLLOR-LOLEDKRENCVLLKIKAD	348
HsCPR	DNAELCIEFGDAIYFCVNPALVNFILKRCGVLDIADOCCEL-SINPK	352
	ISCKIRIYESGDNVAVTPANDSALVWOLCK---ILGADLD--VYNSLHNL	351
HsMTRR	
CeMTRR	TKKXGATLPCHIFACCSLOFIFTVLEIRAIKKAFLRALVDTTSCSAEK	398
HsCPR	TEKIMADIFCHVHKITLHNMFTTCLDIRAFGRPLIRVLAESTDFNEK	402
	DEESKKNHF--FCPTSYRTALTYTLDITNPFRTNVLTELACTASEFSEQ	399
HsMTRR	
CeMTRR	RPLOEL--CSYCGAADYSRFVRDACCLLDLLAFSPCOPPLSLLLENLP	446
HsCPR	RPLELE--CSACGMKDFIDFVTPCLSLADMLFAFPNVKPPVDRLIELLP	450
	ELLKRNASSSGCKELYLSVVVEARRHILALODCPSLRPFIDHLCCELL	449
HsMTRRFAD.....FAD.....FAD.....	
CeMTRR	RLCPKFTSCASSLTFHFGKLNFFVNIVEFLSTATTEVLKCVETGWLALL	496
HsCPR	RLIPKFTSMSS---YENKARLIYSENEFPATOGRRNSRKLATDVLNLSL	497
	RLGARTYSIASSSKVHPNSVHICAVVYETKAGR--INXGVATHNL---	494
HsMTRR	
CeMTRR	VASVLOPHINASHEDSCKALAPKISIPRTTNSFNL-----DDPSLP	539
HsCPR	R-----IGDKVOVLKEFAFRFLPPLGHTKNSACKLP	529
	RAKE-----FVGENGGRALVPMFVRKSOFLPFK-----ATTP	527
HsMTRRNADPH.....	
CeMTRR	ITMVCGTGIAFFIGFLCHREKLCEONPDGNGAMU-LFFGCRNKDRDYL	588
HsCPR	LLMVCGTGVSFVLSFLHFLRLKODSFSDFVDVPRVLFPGROSSVDAL	579
	VIMVCGTGVAFFIGFIOERAULRCOGKE---VGETLLTYGCRSSDEDYL	574
HsMTRRNADPH.....NADPH.....	
CeMTRR	FRKELRNFLKNGILTHLKVSPSRDAFYCEEAFKTYVDONLQDGVAR	638
HsCPR	YHSELEMFVSEGLTDLIICESE-----KGERVCGDLKRYLDKVLP	621
	YREELAGFARDGALTOLNVAFSRE-----GSHKVTVVHLLKODREHLWK	618
HsMTRRNADPH.....	
CeMTRR	ILLOE-NGHITYCGDAKNHAKDVNDALVQIISKEVGVKLEAMKTLATLK	687
HsCPR	FLTAS:ESKIFICGDAKNSKDVOCFSDIVASDOGIPDLEAKKLMOLK	671
	LI--EGGANITYCGDARNHARDVONTFYDIAVELGAMENAGAVDTIKKLM	666
HsMTRRNADPH/FAD.....	
CeMTRR	EEKRYLODIWS	698
HsCPR	KSOQYIEDVWG	682
	TKGRYSLOVWS	677

FIG. 4 page 1 of 2

Protein	Sequence	Position
HsMTRR	
CeMTRR	
HsCPR	50
	
	
HsMTRR	24
CeMTRR	24
HsCPR	100
	
	
HsMTRR	66
CeMTRR	66
HsCPR	146
	
	
HsMTRR	116
CeMTRR	116
HsCPR	193
	
	
HsMTRR	166
CeMTRR	162
HsCPR	233
	
	
HsMTRR	214
CeMTRR	206
HsCPR	271
	
	
HsMTRR	260
CeMTRR	253
HsCPR	293
	
	
HsMTRR	301
CeMTRR	303
HsCPR	306
	
	
HsMTRR	348
CeMTRR	352
HsCPR	351
	
	
HsMTRR	398
CeMTRR	402
HsCPR	399
	
	
HsMTRR	446
CeMTRR	450
HsCPR	449
	
	
HsMTRR	496
CeMTRR	497
HsCPR	494
	
	
HsMTRR	539
CeMTRR	529
HsCPR	527
	
	
HsMTRR	588
CeMTRR	579
HsCPR	574
	
	
HsMTRR	638
CeMTRR	621
HsCPR	618
	
	
HsMTRR	687
CeMTRR	671
HsCPR	666
	
	
HsMTRR	698
CeMTRR	682
HsCPR	677

FIG. 5A

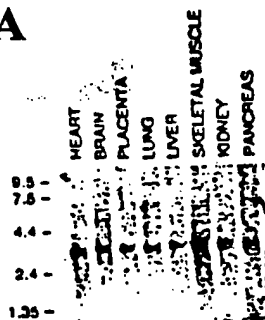


FIG. 5B



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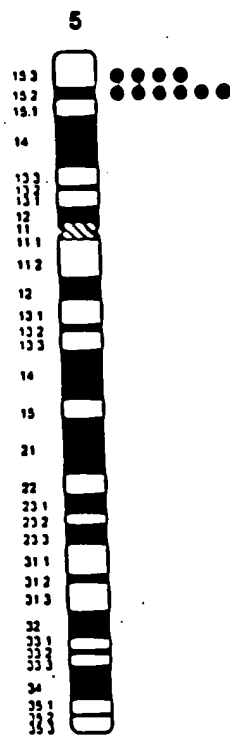


FIG. 6

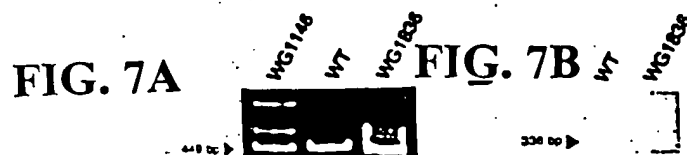


FIG. 7C

Position	Sequence	Accession/ Protein	Organism
572	CAHLYVCCPHHDDVLY	(A025794) HTRB	[H. sapiens]
578	CTHLYVCCPHHDDVLY	(A00537) CPH	[H. sapiens]
588	CTHLYVCCPHHDDVLY	(D00101) CPH	[O. cuniculus]
590	CTHLYVCCPHHDDVLY	(J01090) CPH	[O. solenogaster]
572	CAHLYVCCPHHDDVLY	(P37114) CPH	[V. radialis]
572	CAHLYVCCPHHDDVLY	(J24438) CPH	[A. niger]
1281	CPHLYVCCPHHDDVLY	(U01440) NOS 1	[H. sapiens]
1009	CPHLYVCCPHHDDVLY	(U01440) NOS 11	[H. sapiens]
1040	TPHLYVCCPHHDDVLY	(U01440) NOS 121	[H. sapiens]
180	CPHLYVCCPHHDDVLY	(U01440) NOS	[O. cuniculus]
1009	CPHLYVCCPHHDDVLY	(U01440) NOS	[C. gallus]
481	CPHLYVCCPHHDDVLY	(J01090) SP	[C. coli]
915	CPHLYVCCPHHDDVLY	(J01090) SP	[S. cerevisiae]
407	CPHLYVCCPHHDDVLY	(J01090) SP	[S. cerevisiae]
241	CPHLYVCCPHHDDVLY	(J01090) FNB	[S. cerevisiae]
241	CPHLYVCCPHHDDVLY	(J01090) FNB	[S. cerevisiae]

FIG. 8A

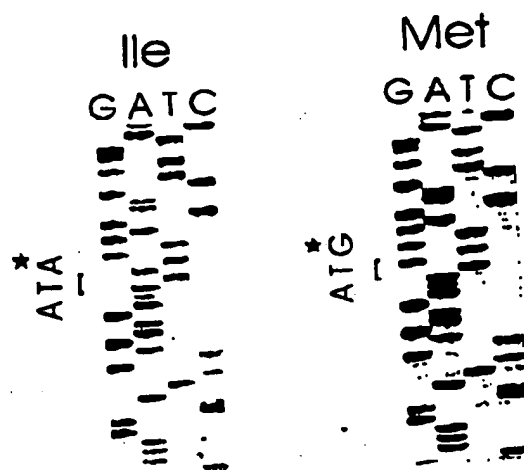


FIG. 8B

